Attorney Docket No. 5849.200-US PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Berka *et al.* Confirmation No. 6980

Serial No.: 09/533,559 Group Art Unit: 1631

Filed: March 22, 2000 Examiner: J.S. Brusca

For: Methods For Monitoring Multiple Gene Expression

DECLARATION UNDER 37 C.F.R. § 1.132

Commissioner for Patents
Washington, DC 20231

Sir:

I, Randy Berka, do hereby state and declare that

1. I am one of the inventors of the subject matter disclosed and claimed in the above-captioned application.

2. I received a Ph.D. in Microbiology and Immunology from the University of Colorado, Health Science Center, Denver, Colorado, in 1983. I have been employed at Novozymes Biotech, Inc., Davis, California, since 1992 where I am currently a Research Fellow.

3. I have read the Office Action dated November 7, 2002 and the Advisory Action dated May 22, 2003 issued in connection with the above-referenced patent application and understand that claims 103-110 have been rejected under 35 U.S.C. § 101 as not supported by a substantial utility. I respectfully disagree with this conclusion.

4. Using Applicants' disclosure in the above-captioned application, one of ordinary skill in the art would be able to set-up and use the methods of the present invention to monitor global expression of a plurality of genes from a filamentous fungal cell with respect to a particular phenotype such as improved secretion or production of a protein or compound, reduced or no secretion or production of a protein or compound, improved or reduced expression of a gene or pathway, desirable morphology, an altered growth rate under desired conditions, relief of over-expression mediated growth inhibition, or tolerance to low oxygen conditions; to discover new genes; to identify possible functions of unknown open reading frames: and to monitor gene copy number variation and stability. For example, the global view of changes in expression of genes may be used to provide a picture of the way in which filamentous fungal cells adapt to changes in culture conditions, environmental stress, or other physiological provocation. Applicants also

provide other possibilities for monitoring global expression including spore formation/germination, recombination, metabolic or catabolic pathway engineering.

5. The experimental study and results described below demonstrate that claims 103-110 are supported by a substantial utility. The study was performed using the protocols described in the above-captioned application.

6. A recombinant *Aspergillus oryzae* strain containing a *Thermomyces lanuginosus* lipase gene (Le-1) and a yield- and morphologically improved mutant (7-1) of Le-1 were analyzed using microarrays containing the *Aspergillus oryzae* ESTs disclosed in the above-captioned application. When Le-1 is grown in laboratory fermentors it displays a very pronounced "ballooning" phenotype where the mycelium becomes bloated and fragmented After approximately 90 hours of fermentation the culture undergoes a significant morphological change and becomes more viscous. Concomitantly the dissolved air tension drops rapidly and production of the lipase ceases. Mutant 7-1 was isolated as a classical mutant of Le-1 by mutagenesis and high-throughput screening. This mutant displays a much lower degree of ballooning and does not display the catastrophic changes in fermentation morphology and productivity. The initial productivity of 7-1 is similar to that of Le-1, but, in contrast to Le-1, does not stop producing lipase after 90 hours.

7. Samples of mRNA extracted from strains Le-1 and 7-1 cultivated in 1 L fermentors for 3 or 4 days were labeled and hybridized to a microarray containing the *Aspergillus oryzae* ESTs described in Appendix A. Each strain was fermented twice yielding a total of 4 samples per strain for microarray analysis. In each hybridization mRNAs from Le-1 and 7-1 were labeled with different fluorophores, mixed, and hybridized to the slide. Samples from Le-1 (day 3) were compared to samples from 7-1 (day 3), and samples from the two strains at four days post inoculum were also compared. A total of 5 hybridizations were performed with mRNA extracted from day 3 samples, and 2 hybridizations were performed with mRNA extracted from day 4 samples. The samples from each strain at day 4 were from the same fermentation and thus represent technical replicates rather than biological replicates. Microarray slides from the hybridizations were scanned and the image data analyzed as described in the above-captioned application. The data from each time point were used as replicates for the identification of significantly differentially regulated genes on a 95% confidence level. This yielded a list of differentially regulated genes from each time point (shown in Appendix A).

8. Analysis revealed a number of genes whose transcript levels differed between the strains. Among these genes were 53 ribosomal genes and 27 genes identified as being involved in cell wall synthesis and morphogenesis, indicating that general protein production and the cell wall metabolism is regulated differently in the strains. These results fit well with the observation that the morphology of the two strains is different, especially with regard to the degree of "ballooning" when expressing the lipase gene.

9 From the list in Appendix A, it is obvious that the ribosomal genes are differentially expressed between the two strains. The 53 ribosomal genes are consistently down-regulated in 7-1 compared to Le-1 on both day 3 and day 4. Similarly, three genes with homology to the translation initiation factor 3 from *Schizosaccharomyces pombe* are down-regulated in 7-1 while 5 of 6 genes with homology to tRNAs are up-regulated in 7-1. The consistent down-regulation of genes involved in translation indicates that 7-1 has generally reduced translational activity compared to Le-1, which may relieve some of the secretional stress and reduce the degree of ballooning seen in Le-1. It may also reduce the counter-selective pressure against lipase-producing cells that may be responsible for the rapid loss of expression potential in Le-1

cultures after 90 hours of fermentation, allowing 7-1 to retain its expression potential throughout the fermentation. Another explanation could be that the growth rate of the 7-1 cells are lower that that of Le-1. The cultures are dosed approximately the same amount of glucose during fermentation, but the Le-1 culture changes composition rather abruptly in the period leading up to the 90 hours time point. The Le-1 cells that produce lipase become inactive and ultimately die while the culture is taken over by cells that have lost lipase production capacity.

10. The list of differentially regulated genes in Appendix A shows 27 genes involved in cell-wall synthesis. Twenty of these genes are consistently up-regulated while seven are down-regulated in 7-1 compared to Le-1. Figure 1 shows a model for the synthesis of β-glucans in the cell wall of fungi. Some of the genes listed in Appendix A can be assigned (by homology to genes of known or putative function) to the first three steps of cell wall synthesis as depicted in Figure 1. Among the genes that can be assigned to the first step, biosynthesis of linear 1,3-β-glucans, is a homolog of FSK (*Aspergillus fumigatus*, Kelly *et al.* 1996, *J. Bact.* 178: 4381-4391; Beauvais *et al.* 2001, *J. Bact.* 183: 2273-2279), RHO2 (regulator of α-glucan biosynthesis in *S. pombe*, Hirata *et. al.* 1998, *J. Cell Sci.* 111: 149-159), RHO-GTPase (same family of proteins as RHO2), and RHO GDP dissociation inhibitor (Sasaki & Takai, 1998, *J. Bact.* 183: 2273-2279). FSK and RHO2 are up-regulated while the RHO GDP dissociation inhibitor is down-regulated. The results suggest that the β-glucan synthesis pathway is up-regulated.

11. Two of the differentially regulated genes in Appendix A can be assigned to the second step in the biosynthesis of β-glucan, namely a protein with homology to a *Fusarium venenatum* glucanase and a protein with homology to an *Aspergillus fumigatus* β-1,3-glucanolsyltransferase. Both proteins have homology to the Bgl2 protein from *Saccharomyces cerevisiae*. The *Aspergillus fumigatus* homolog have been shown to introduce intrachain 1,6-β-lingages into 1,3-β-glucan, although the role of the *Aspergillus fumigatus* protein in cell wall synthesis is yet unclear (Mouyna *et al.*, 1998, *Microbiology* 144: 3171-3180).

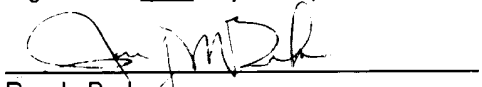
12. Five genes from Appendix A can be assigned to the third step in the pathway shown in Figure 1. Each of these genes has homology to one of the three GEL genes identified in *Aspergillus fumigatus* (Mouyna *et. al.*, 2000, *J. Biol. Chem.* 275: 14882-14889; Mouyna *et. al.*, 2000, *Biochem. J.* 347: 741-747). The GEL1p protein is the most intensively studied enzyme of the three and encodes a glycosylphosphatidylinositol-anchored β-1,3-glucanosyltransferase that cleaves a β-1,3-glucan internally and transfers the reducing end to the non-reducing end of another β-1,3-glucan molecule, resulting in elongation of this glucan chain. While deletion of the GEL1p protein does not confer a phenotype to *Aspergillus fumigatus*, a GEL2p mutant has a reduced growth rate and altered conidiation. The GEL3p protein is not expressed in standard culture conditions (Bernard and Latgé, 2001, *Med. Mycol.* 39, suppl. I, 9-17). In strain 7-1 the GEL1p and GEL2p homologues are up-regulated, but the GEL3p homologues are down-regulated. The regulation patterns of the differentially expressed genes involved in cell-wall synthesis suggest that the β-glucan synthesis pathway is up-regulated in strain 7-1 compared to Le-1. The physiological effect of the increased activity of this pathway is consistent with the reduced ballooning seen in 7-1, since it may be that the ballooning phenotype could be caused by a deficiency of cell-wall components at the hyphae elongation sites, and that this deficiency could be an effect of immense overloading of the secretion machinery in the cells. While the up-regulation of proteins that take part in cell-wall synthesis *in situ* does not reduce the pressure on the secretion pathway, it may increase the secretion of cell-wall synthesis enzymes at the expense of other, less crucial, enzymes.

12. The results described above clearly demonstrate that the microarrays produced from the

Aspergillus oryzae ESTs provide a powerful tool to study the effect of strain differences on global gene expression in the cells. Especially in the context of mutants produced by "classical" means (*i.e.*, by radiation or chemical mutagenesis) the microarray analysis provides one of the very few methods for identifying the genetic targets of the mutagens. Without this technique it would be an almost impossible task to identify the pathways and ideally the genes that are affected by the introduced mutations.

13. The undersigned declarant declares further that all statements made herein of her own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize any patent issuing thereon.

Signed this 16 day of September 2003



Randy Berka

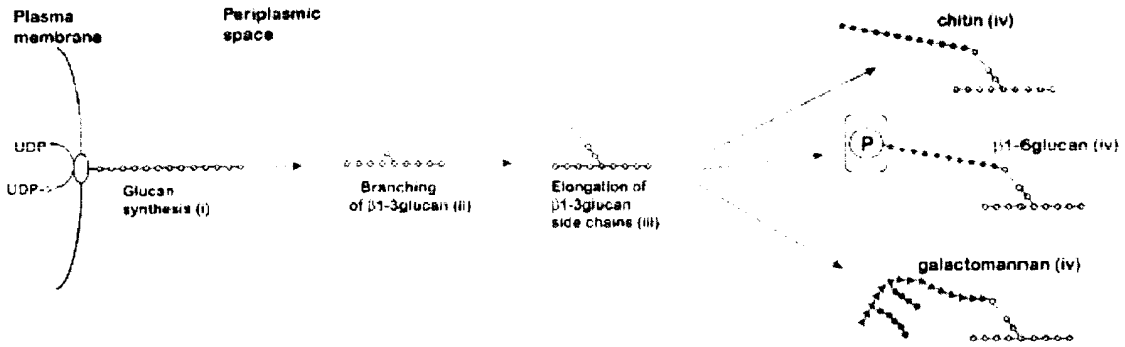


Figure 1. Chronological events involved in the synthesis and postsynthetic modifications of the cell wall 1,3-β-glucans. (i) Biosynthesis of linear 1,3-β-glucan; (ii) branching of 1,3-β-glucans through 1,6-β-glucan side chains; (iii) elongation of 1,3-β-glucan side chains; and (iv) cross-linking of other polymers (chitin and galactomannan in *A. fumigatus*, or chitin, 1,6-β-glucan, and proteins in *S. cerevisiae*) onto non-reducing ends of 1,3-β-glucan side chains. *P*, proteins. From Mouyna *et al.* 2000a.

Appendix A

Differentially expressed genes in 7-1 compared to Le-1 on day 3 and day 4.

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:Q9P380 Schizosaccharomyces pombe PUTATIVE PEPTIDE TRANSPORTER.	AA-transport	2,8	2,6
SWISSPROT:P19145 Saccharomyces cerevisiae General amino-acid permease GAP1.	AA-transport	2,6	3,4
SWISSPROT:P53388 Saccharomyces cerevisiae Dicarboxylic amino acid permease.	AA-transport	2,5	3,1
SWISSPROT:P53090 Saccharomyces cerevisiae Aromatic amino acid aminotransferase I (EC 2.6.1.-).	AA-transport	1,4	2,1
SWISSPROT:P38090 Saccharomyces cerevisiae General amino acid permease AGP2.	AA-transport	1,3	1,8
TREMBL:Q96W94 Saccharomyces kluyveri (EC=3.5.1.6) BETA-ALANINE SYNTHASE (EC 3.5.1.6).	AA-metabolism	3,6	2,2
SWISSPROT:Q92413 Emericella nidulans (EC=2.6.1.13) Ornithine aminotransferase (EC 2.6.1.13) (Ornithine--oxo-aci	AA-metabolism	2,1	3,1
TREMBL:Q96V52 Emericella nidulans (EC=6.3.1.2) GLUTAMINE SYNTHETASE (EC 6.3.1.2).	AA-metabolism	1,9	2,4
TREMBL:Q93H39 Streptomyces avermitilis NON-RIBOSOMAL PEPTIDE SYNTHETASE.	AA-metabolism	1,7	1,2
TREMBL:Q9Y7G4 Emericella nidulans CARNITINE/ACYL CARNITINE CARRIER.	AA-metabolism	1,6	1,5
TREMBL:Q9P8T7 Paracoccidioides brasiliensis ORNITHINE DECARBOXYLASE.	AA-metabolism	1,5	1,3
SWISSPROT:Q12611 Emericella nidulans (EC=3.5.3.1) Arginase (EC 3.5.3.1).	AA-metabolism	1,4	1,5
TREMBL:Q9Y7B2 Emericella nidulans (EC=5.4.99.5) CHORISMATE MUTASE (EC 5.4.99.5).	AA-metabolism	1,4	1,4
SWISSPROT O74787 Schizosaccharomyces pombe (EC=2.1.1.17) Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) (	AA-metabolism	1,4	1,4
TREMBL O42652 Schizosaccharomyces pombe (EC=2.6.1.1) PUTATIVE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1	AA-metabolism	-1,3	-3,1
SWISSPROT P17324 Saccharomyces cerevisiae (EC=4.2.1.13) L-serine dehydratase (EC 4.2.1.13) (L-serine deaminase).	AA-metabolism	-1,5	-10,7
TREMBL Q9HFU6 Emericella nidulans ORNITHINE DECARBOXYLASE ANTIZYME.	AA-metabolism	-1,6	-2,1
TREMBL Q96WX7 Emericella nidulans (EC=1.5.1.2) PUTATIVE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2).	AA-metabolism	-1,7	-1,6
TREMBL Q9P444 Emericella nidulans (EC=2.1.1.14) COBALAMIN-INDEPENDENT METHIONINE SYNTHASE (EC 2.1.1.14).	AA-metabolism	-1,8	-1,8
TREMBL Q9Y7N4 Schizosaccharomyces pombe (EC=1.4.3.3) PUTATIVE D-AMINO ACID OXIDASE (EC 1.4.3.3) (DAMOX) (DAO) (DA	AA-metabolism	-1,9	-1,3
TREMBL Q8X0I9 Neurospora crassa KETOL-ACID REDUCTOISOMERASE (ILV-2).	AA-metabolism	-2,4	-1,9
SWISSPROT P38088 Saccharomyces cerevisiae (EC=6.1.1.14) Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase)	tRNA	1,9	1,4
SWISSPROT P09880 Saccharomyces cerevisiae (EC=6.5.1.3) tRNA ligase (EC 6.5.1.3).	tRNA	1,7	1,4
SWISSPROT O42870 Schizosaccharomyces pombe (EC=6.1.1.20) Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phen	tRNA	1,5	1,4
TREMBL CAD37006 Neurospora crassa Probable tma splicing protein spl1.	tRNA	1,5	1,5
TREMBL O74781 Schizosaccharomyces pombe (EC=6.1.1.19) PUTATIVE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19)(	tRNA	1,4	1,6
SWISSPROT P04802 Saccharomyces cerevisiae (EC=6.1.1.12) Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12) (Asparta	tRNA	-1,5	-1,2
SWISSPROT:Q12207 Saccharomyces cerevisiae Non-classical export protein 2.	Transport	-3,6	-4,4
SWISSPROT:O14164 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 93 kDa s	translation	-1,3	-1,3
SWISSPROT:O59742 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 135 kDa	translation	-1,6	-1,8
SWISSPROT:O59742 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 135 kDa	translation	-2,2	-1,4
SWISSPROT:Q9UST4 Schizosaccharomyces pombe Initiation factor 5A-2 (eIF-5A 2).	Transcription	2,3	1,4
TREMBL Q9P3D9 Neurospora crassa RELATED TO GTP-BINDING PROTEIN RAB2.	Transcription	2,3	2,0
SWISSPROT:Q12753 Saccharomyces cerevisiae Transcriptional activator HAA1.	Transcription	1,7	1,2
TREMBL:Q9HEX7 Pneumocystis carinii HELIX-LOOP-HELIX DNA BINDING PROTEIN	Transcription	1,5	1,4
TREMBL:AAM22470 Fusarium solani Cutinase transcription factor 1 alpha	Transcription	1,4	1,3
SWISSPROT:Q12731 Emericella nidulans Transcription initiation factor TFIID (TATA-box factor) (TAT	Transcription	1,3	1,6
SWISSPROT:P08153 Saccharomyces cerevisiae Transcriptional factor SWI5.	Transcription	1,3	2,4
TREMBL:O59849 Aspergillus oryzae HAPE.	Transcription	1,3	1,5
TREMBL:Q00069 Ascobolus immersus ZINC FINGER PROTEIN.	Transcription	-1,2	-2,4
SWISSPROT:P49373 Schizosaccharomyces pombe Transcription elongation factor S-II (TFIIS).	Transcription	-1,3	-1,3
SWISSPROT:Q92371 Schizosaccharomyces pombe Transcription factor BTF3 homolog.	Transcription	-1,4	-1,3
SWISSPROT:P47943 Schizosaccharomyces pombe Eukaryotic initiation factor 4A (eIF-4A) (eIF4A).	Transcription	-2,1	-1,4
SWISSPROT:Q92794 Homo sapiens Monocytic leukemia zinc finger protein (Zinc finger protein	Transcription	-2,2	-5,5

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
GENESEQP:AAE06000 Unidentified Zinc finger protein (ZFP) m1 protein.	Transcription	-2,6	-23,0
TREMBL:Q96WT5 Aspergillus oryzae MALTOSE PERMEASE.	sugar-transport	3,6	6,3
ERDBP:NP000895 Fusarium oxysporum F. oxysporum Glucose Transporter	sugar-transport	1,9	9,5
SWISSPROT:P15325 Emericella nidulans Quinate permease (Quinate transporter).	sugar-transport	1,8	1,5
TREMBL:Q9P3B9 Neurospora crassa RELATED TO MYO-INOSITOL TRANSPORT PROTEIN ITR1.	sugar-transport	-1,2	-1,9
SWISSPROT:Q92253 Neurospora crassa Probable glucose transporter rco-3.	sugar-transport	-2,0	-3,9
SWISSPROT:Q92253 Neurospora crassa Probable glucose transporter rco-3.	sugar-transport	-6,2	-5,1
SWISSPROT:Q9USI5 Schizosaccharomyces pombe Heat shock protein sti1 homolog.	Stress	1,8	2,4
SWISSPROT:P23724 Saccharomyces cerevisiae (EC=3.4.25.1) Potential proteasome component C5 (EC 3.4.25.1) (Multicataly	Stress	1,6	1,6
TREMBL:Q8X041 Neurospora crassa RELATED TO HSP90 ASSOCIATED CO-CHAPERONE.	Stress	1,6	2,4
TREMBL:Q9HGT8 Coccidioides immitis UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (FRAGMENT)	stress	1,4	2,3
SWISSPROT:O74225 Neurospora crassa Heat shock protein Hsp88.	stress	1,3	1,7
TREMBL:Q9P5S4 Neurospora crassa RELATED TO HSP70 PROTEIN.	stress	1,3	2,6
SWISSPROT:O74225 Neurospora crassa Heat shock protein Hsp88.	stress	-1,4	-1,5
GENESEQP:AAR43654 Aspergillus nidulans c424 gene product.	Stress	-2,3	-3,7
GENESEQP:AAR43654 Aspergillus nidulans c424 gene product.	Stress	-2,9	-2,8
SWISSPROT:P18899 Saccharomyces cerevisiae DDR48 stress protein (DNA damage-responsive protein 48) (DDR	Stress	-3,0	-3,5
TREMBL:Q9HG46 Aspergillus oryzae PUTATIVE 3-KETOACYL-COA THIOLASE.	Sterol/Lipid met	1,4	1,2
TREMBL:Q29517 Oryctolagus cuniculus (EC=3.1.4.11) PHOSPHOLIPASE C (EC 3.1.4.11) (FRAGMENT).	Sterol/Lipid met	-1,2	-2,1
GENESEQP:AAB19184 Saccharomyces cerevisiae Lipid metabolism protein encoded by the open reading frame Y	Sterol/Lipid met	-1,4	-1,3
SWISSPROT:O59933 Candida albicans C-4 methyl sterol oxidase (EC 1 - - -)	Sterol/Lipid met	-1,6	-6,2
SWISSPROT:O14340 Schizosaccharomyces pombe Oxysterol-binding protein homolog C2F12.05c.	Sterol/Lipid met	-1,8	-3,2
TREMBL:Q9P8R0 Aspergillus fumigatus CYTOCHROME P450 STEROL 14 ALPHA-DEMETHYLASE (14-ALPHA STEROL	Sterol/Lipid met	-2,3	-45,4
TREMBL:Q9P3J7 Neurospora crassa RELATED TO SPORE COAT PROTEIN SP96.	Sporulering	-1,4	-1,2
TREMBL:Q9P3J7 Neurospora crassa RELATED TO SPORE COAT PROTEIN SP96	Sporulering	-2,2	-1,9
TREMBL:Q96UP0 Neurospora crassa PHEROMONE PPG-1-LIKE PROTEIN (PHEROMONE PRECURSOR).	signalling	4,1	20,3
TREMBL:Q9GYW6 Drosophila melanogaster THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN TRAP170 (FRAGMEN	signalling	1,6	1,5
TREMBL:O74749 Schizosaccharomyces pombe SIMILARITY TO MAMMALIAN SIGNAL TRANSDUCING ADAPTOR.	signalling	-1,9	-2,6
TREMBL:Q9JLE9 Rattus norvegicus GABA-A RECEPTOR EPSILON-LIKE SUBUNIT.	signalling	-2,8	-35,8
SWISSPROT:Q04491 Saccharomyces cerevisiae Protein transport protein SEC13.	secretion	1,7	1,9
ERDBP:NP000597 Fusarium venenatum F. venenatum GDI homolog	secretion	1,4	1,6
TREMBL:Q8X0K7 Neurospora crassa RELATED TO SECRETORY PROTEIN SSP120.	secretion	-1,3	-3,1
SWISSPROT:P53619 Bos taurus Coatomer delta subunit (Delta-coat protein) (Delta-COP).	secretion	-1,6	-1,5
TREMBL:Q8X079 Neurospora crassa RELATED TO RNA HELICASE/RNASEIII CAF.	RNA	1,7	1,3
TREMBL:O00870 Trypanosoma brucei RIBONUCLEASE H1.	RNA	1,6	1,2
TREMBL:Q9CWZ3 Mus musculus 2310057C03RIK PROTEIN (RNA BINDING MOTIF PROTEIN 8A).	RNA	1,3	2,1
SWISSPROT:Q07478 Saccharomyces cerevisiae Probable ATP-dependent RNA helicase SUB2.	RNA	1,3	1,7
TREMBL:Q9Y7A8 Neurospora crassa PAD-1.	RNA	1,3	1,9
TREMBL:Q9P3U1 Schizosaccharomyces pombe PROTEIN WITH 3 RNA BINDING DOMAINS, YEAST HRB1 HOMOLOGUE.	RNA	-1,3	-1,4
TREMBL:Q9P3E1 Neurospora crassa RELATED TO RNA-BINDING PROTEIN FUS/TLS.	RNA	-1,3	-1,7
TREMBL:Q9UQ35 Homo sapiens RNA BINDING PROTEIN	RNA	-1,8	-1,3
SWISSPROT:O74330 Schizosaccharomyces pombe 40S ribosomal protein S27	Ribosomal	-1,2	-1,6
SWISSPROT:P53163 Saccharomyces cerevisiae Putative 60S ribosomal protein L7/L12 homolog, mitochondrial	Ribosomal	-1,2	-1,7
SWISSPROT:P23369 Saccharomyces cerevisiae Mitochondrial 60S ribosomal protein L25 (YmL25)	Ribosomal	-1,3	-1,4
SWISSPROT:Q10157 Schizosaccharomyces pombe 60S ribosomal protein L11.	Ribosomal	-1,4	-1,4
SWISSPROT:O42952 Schizosaccharomyces pombe 40S ribosomal protein S30.	Ribosomal	-1,4	-1,4
SWISSPROT:P49631 Saccharomyces cerevisiae 60S ribosomal protein L43 (L37A) (YL35)	Ribosomal	-1,4	-1,7
SWISSPROT:Q9P3T6 Schizosaccharomyces pombe 40s ribosomal protein S5-B.	Ribosomal	-1,4	-1,5
SWISSPROT:O74836 Schizosaccharomyces pombe 60S ribosomal protein L1-B (L10a).	Ribosomal	-1,5	-2,6

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
SWISSPROT:Q9C0T1 Emericella nidulans 60S ribosomal protein L37.	Ribosomal	-1,5	-1,3
SWISSPROT:O60128 Schizosaccharomyces pombe 40S ribosomal protein S3.	Ribosomal	-1,5	-1,6
SWISSPROT:O74172 Schizosaccharomyces pombe 40S ribosomal protein S25-B (S31-B).	Ribosomal	-1,5	-2,0
SWISSPROT:O59953 Neurospora crassa 60S ribosomal protein L5 (CPR4).	Ribosomal	-1,6	-1,4
SWISSPROT:P34737 Podospora anserina 40S ribosomal protein S15 (S12).	Ribosomal	-1,6	-1,5
SWISSPROT:Q9HFR7 Trichoderma hamatum 60S ribosomal protein L36 (TRP36).	Ribosomal	-1,6	-1,3
SWISSPROT:P78987 Erysiphe graminis 60S ribosomal protein L27A (L29).	Ribosomal	-1,6	-1,5
SWISSPROT:P26781 Saccharomyces cerevisiae 40S ribosomal protein S11 (S18) (YS12) (RP41).	Ribosomal	-1,7	-1,7
SWISSPROT:O13672 Schizosaccharomyces pombe 60S ribosomal protein L8 (L7A) (L4).	Ribosomal	-1,7	-1,7
TREMBL:Q9P4Z0 Neurospora crassa PROBABLE RIBOSOMAL PROTEIN RPS8BP.	Ribosomal	-1,7	-1,3
SWISSPROT:Q9HE25 Neurospora crassa 60S ribosomal protein L17.	Ribosomal	-1,7	-1,8
SWISSPROT:Q9USX4 Schizosaccharomyces pombe 60S ribosomal protein L33-A (L37A).	Ribosomal	-1,7	-1,6
SWISSPROT:P21772 Neurospora crassa 40S ribosomal protein S26E (CRP5) (13.6 kDa ribosomal protei	Ribosomal	-1,8	-1,4
TREMBL:Q9C2B9 Neurospora crassa PROBABLE RIBOSOMAL PROTEIN L38.	Ribosomal	-1,8	-1,9
SWISSPROT:P04451 Saccharomyces cerevisiae 60S ribosomal protein L23 (L17).	Ribosomal	-1,8	-1,3
SWISSPROT:O13418 Aspergillus niger 60S ribosomal protein L15.	Ribosomal	-1,8	-1,8
TREMBL:Q9C2H7 Neurospora crassa PROBABLE RIBOSOMAL PROTEIN RPL4A.	Ribosomal	-1,8	-1,5
SWISSPROT:P21772 Neurospora crassa 40S ribosomal protein S26E (CRP5) (13.6 kDa ribosomal protei	Ribosomal	-1,9	-1,5
SWISSPROT:P79015 Schizosaccharomyces pombe 60S ribosomal protein L32-A.	Ribosomal	-1,9	-2,0
SWISSPROT:Q9P7B2 Schizosaccharomyces pombe 40S ribosomal protein S8-B.	Ribosomal	-1,9	-1,7
TREMBL:Q9HGV0 Aspergillus fumigatus ACIDIC RIBOSOMAL PROTEIN P1.	Ribosomal	-2,0	-1,4
TREMBL:Q96W54 Candida albicans RIBOSOMAL PROTEIN S22.	Ribosomal	-2,0	-1,8
SWISSPROT:P05736 Saccharomyces cerevisiae 60S ribosomal protein L2 (YL6) (L5) (RP8).	Ribosomal	-2,1	-1,2
TREMBL:Q9USW5 Schizosaccharomyces pombe 40S RIBOSOMAL PROTEIN S4-2.	Ribosomal	-2,1	-1,3
TREMBL:Q9C2B9 Neurospora crassa PROBABLE RIBOSOMAL PROTEIN L38.	Ribosomal	-2,1	-5,1
SWISSPROT:O60143 Schizosaccharomyces pombe 60S ribosomal protein L7-C.	Ribosomal	-2,1	-1,6
SWISSPROT:Q10421 Schizosaccharomyces pombe 40S ribosomal protein S28 (S33).	Ribosomal	-2,2	-1,6
TREMBL:Q96UT5 Paracoccidioides brasiliensis PUTATIVE RIBOSOMAL PROTEIN L35.	Ribosomal	-2,2	-1,5
TREMBL:Q9C3Z6 Podospora anserina RIBOSOMAL PROTEIN P0.	Ribosomal	-2,2	-1,3
SWISSPROT:P36105 Saccharomyces cerevisiae 60S ribosomal protein L14-A.	Ribosomal	-2,2	-1,5
SWISSPROT:P52810 Podospora anserina 40S ribosomal protein S9 (S7).	Ribosomal	-2,2	-1,6
TREMBL:Q9URK4 Schizosaccharomyces pombe RIBOSOMAL PROTEIN S16 HOMOLOG (FRAGMENT).	Ribosomal	-2,3	-1,3
TREMBL:Q9HDQ7 Colletotrichum gloeosporioides PUTATIVE 60S RIBOSOMAL PROTEIN.	Ribosomal	-2,3	-1,9
SWISSPROT:O59953 Neurospora crassa 60S ribosomal protein L5 (CPR4).	Ribosomal	-2,3	-1,5
TREMBL:CAD37159 Aspergillus fumigatus Putative ribosomal protein.	Ribosomal	-2,3	-1,3
SWISSPROT:O14069 Schizosaccharomyces pombe Probable 60S ribosomal protein C1687.06c.	Ribosomal	-2,4	-1,3
TREMBL:AAM43909 Aspergillus fumigatus Large subunit ribosomal protein L3.	Ribosomal	-2,4	-1,5
TREMBL:CAA37766 Neurospora crassa Ribosomal protein crp-2.	Ribosomal	-2,4	-2,1
SWISSPROT:Q09668 Schizosaccharomyces pombe 60S ribosomal protein L22.	Ribosomal	-2,4	-2,2
TREMBL:Q96W42 Ophiostoma novo-ulmi RIBOSOMAL PROTEIN L34-LIKE PROTEIN.	Ribosomal	-2,4	-2,0
SWISSPROT:P27073 Emericella nidulans 40S ribosomal protein S19 (S16).	Ribosomal	-2,4	-1,9
SWISSPROT:O74892 Schizosaccharomyces pombe 40S ribosomal protein S2.	Ribosomal	-2,6	-1,2
TREMBL:Q9UVN8 Emericella nidulans RIBOSOMAL PROTEIN L16A.	Ribosomal	-2,7	-1,5
SWISSPROT:Q10192 Schizosaccharomyces pombe 60S ribosomal protein L18.	Ribosomal	-2,7	-1,4
SWISSPROT:O74893 Schizosaccharomyces pombe 40S ribosomal protein S20.	Ribosomal	-2,7	-1,6
SWISSPROT:Q9C0Z7 Schizosaccharomyces pombe 40S ribosomal protein S6-B.	Ribosomal	-2,7	-1,4
TREMBL:Q9HFB3 Aspergillus oryzae PACC.	regulenng	2,4	1,3
TREMBL:Q9UVK6 Emericella nidulans MITOGEN-ACTIVATED PROTEIN KINASE.	regulenng	2,1	1,3
TREMBL:Q9HET3 Aspergillus niger SECRETION RELATED GTPASE (SRGB).	regulering	1,8	2,2
TREMBL:Q9Y899 Emericella nidulans CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE B.	regulering	1,7	1,3
TREMBL:Q9P5Z9 Neurospora crassa RELATED TO NIF-SPECIFIC REGULATORY PROTEIN.	regulenng	1,5	1,7
SWISSPROT:P36586 Schizosaccharomyces pombe Ras-related protein ypt5.	regulenng	1,5	1,4

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:O74251 Emericella nidulans MEDUSA.	regulering	1,4	1,9
SWISSPROT:P87072 Neurospora crassa Calcineurin B subunit (Protein phosphatase 2B regulatory sub	regulering	1,4	1,9
TREMBL:Q8WZR7 Neurospora crassa PROBABLE GTP-BINDING PROTEIN DRAB11.	regulering	1,3	1,9
TREMBL:Q9C297 Neurospora crassa RAS-2 PROTEIN.	regulering	-1,3	-1,9
SWISSPROT:Q00771 Emericella nidulans (EC=2.7.1.123) Calcium/calmodulin-dependent protein kinase (EC 2.7.1.123) (	Regulering	-2,2	-1,3
TREMBL:Q10294 Schizosaccharomyces pombe CAMP-INDEPENDENT REGULATORY PROTEIN PAC2.	Regulering	-3,4	-8,4
GENESEQP:ABP60744 Aspergillus nidulans Aspergillus nidulans thioredoxin SEQ ID NO:93.	redox	-1,2	-2,1
TREMBL:Q9HFR2 Ajellomyces capsulata PUTATIVE THIOL-SPECIFIC ANTIOXIDANT PROTEIN TSA1.	redox	-1,3	-2,3
TREMBL:Q9P5T9 Neurospora crassa PROBABLE NI-BINDING UREASE ACCESSORY PROTEIN (UREG).	purine/pyrimidine metabolism	1,7	1,5
TREMBL:BAC07276 Neurospora crassa (EC=6.3.2.6) 5'-phosphoribosyl-5-aminoimidazole-4-N-succinoca rboxamide s	purine/pyrimidine metabolism	-1,3	-1,6
TREMBL:Q12610 Emericella nidulans (EC=1.3.1.14) DIHYDROOROTATE DEHYDROGENASE (EC 1.3.1.14).	purine/pyrimidine metabolism	-1,4	-1,6
TREMBL:CAD37041 Neurospora crassa Nucleoside-diphosphate kinase.	purine/pyrimidine metabolism	-1,7	-2,2
TREMBL:Q9UTG1 Schizosaccharomyces pombe PUTATIVE PURINE NUCLEOSIDE PHOSPHORYLASE.	purine/pyrimidine metabolism	-2,2	-1,6
TREMBL:Q8X175 Emericella nidulans KARYOPHERIN ALPHA.	protein transport nucleus	-1,4	-1,4
TREMBL:O93914 Aspergillus niger PDI RELATED PROTEIN A.	Protein folding	2,9	5,9
TREMBL:Q9C2N6 Neurospora crassa RELATED TO DNAJ-LIKE PROTEIN HOMOLOG.	Protein folding	1,9	1,8
TREMBL:Q9HGM9 Schizosaccharomyces pombe DNAJ DOMAIN PROTEIN SIMILAR TO HUMAN TETRATRICOPEPTIDE REPEA	Protein folding	1,8	1,2
TREMBL:Q8X0V3 Neurospora crassa PROBABLE PEROXISOMAL PROTEIN POX18.	peroxisom	1,6	1,8
TREMBL:Q8WZW4 Neurospora crassa RELATED TO PEROXISOMAL MEMBRANE PROTEIN PMP47B.	peroxisom	-1,7	-2,1
TREMBL:Q59632 Ochrobactrum anthropi (EC=3.4.11.19) D-AMINOPEPTIDASE (EC 3.4.11.19).	peptidase/protease	3,2	5,1
TREMBL:Q96VC4 Emericella nidulans CARBOXYPEPTIDASE.	peptidase/protease	1,9	1,6
TREMBL:Q96VT2 Aspergillus niger (EC=3.4.11.5) PROLYL AMINOPEPTIDASE A (EC 3.4.11.5).	peptidase/protease	1,5	2,4
TREMBL:Q98L22 Rhizobium loti PROLINE DIPEPTIDASE.	peptidase/protease	1,3	2,4
TREMBL:Q9UUR7 Metarhizium anisopliae METALLOPROTEASE MEP1.	peptidase/protease	-1,5	-1,4
TREMBL:AAM55216 Alcaligenes eutrophus 6-chlorohydroxyquinol-1,2-dioxygenase.	Mitochondriel	3,0	1,5
SWISSPROT:P14187 Neurospora crassa (EC=4.4.1.17) Cytochrome c heme lyase (EC 4.4.1.17) (CCHL) (Holocytochrome	Mitochondriel	2,2	1,3
TREMBL:Q8WZY6 Neurospora crassa PROBABLE COPROPORPHYRINOGEN OXIDASE.	Mitochondriel	1,7	1,9
SWISSPROT:P00431 Saccharomyces cerevisiae (EC=1.11.1.5) Cytochrome C peroxidase, mitochondrial precursor (EC 1.11.1.	Mitochondriel	1,4	2,3
SWISSPROT:Q07536 Bos taurus (EC=1.2.1.27) Methylmalonate-semialdehyde dehydrogenase [acylating], mitoc	Mitochondriel	1,4	1,8
TREMBL:Q9Y857 Kluyveromyces lactis (EC=1.1.2.3) CYTOCHROME B2 PRECURSOR (EC 1.1.2.3)	Mitochondriel	1,4	3,7
TREMBL:O74752 Schizosaccharomyces pombe PUTATIVE MITOCHONDRIAL PROTEIN IMPORT PROTEIN.	Mitochondriel	1,3	2,2
SWISSPROT:Q9Y8A7 Emericella nidulans Mitochondrial import inner membrane translocase subunit TIM9	Mitochondriel	-1,2	-1,8
SWISSPROT:P39515 Saccharomyces cerevisiae Mitochondrial import inner membrane translocase subunit TIM1	Mitochondriel	-1,2	-1,7
SWISSPROT:P38364 Fusarium solani Pisatin demethylase (EC 1.14.-.-) (Cytochrome P450 57A2).	Mitochondriel	-1,2	-2,0
SWISSPROT:Q9UUZ9 Aspergillus oryzae Thiazole biosynthetic enzyme, mitochondrial precursor.	Mitochondriel	-1,2	-2,2
TREMBL:P87230 Schizosaccharomyces pombe PUTATIVE UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE C4G3.04C(	Mitochondriel	-1,3	-1,4
TREMBL:Q94EK6 Pisum sativum FERRIC-CHELATE REDUCTASE.	Mitochondriel	-1,3	-1,6
TREMBL:Q8WZW6 Neurospora crassa RELATED TO ATP SYNTHASE EPSILON CHAIN (MITOCHONDRIAL).	Mitochondriel	-1,3	-1,3
SWISSPROT:O74471 Schizosaccharomyces pombe Cytochrome c oxidase polypeptide via. mitochondrial precurso	Mitochondriel	-1,3	-2,1
SWISSPROT:Q12233 Saccharomyces cerevisiae (EC=3.6.3.14) ATP synthase G chain, mitochondrial (EC 3.6.3.14)	Mitochondriel	-1,3	-1,9
TREMBL:BAC10043 Oryza sativa Putative cytochrome P450.	Mitochondriel	-1,3	-1,3
SWISSPROT:O13350 Kluyveromyces lactis (EC=3.6.3.14) ATP synthase D chain, mitochondrial (EC 3.6.3.14).	Mitochondriel	-1,3	-1,5
TREMBL:Q9C1X2 Schizosaccharomyces pombe PUTATIVE D-LACTATE DEHYDROGENASE MITOCHONDRIAL	Mitochondriel	-1,4	-2,6
SWISSPROT:P17505 Saccharomyces cerevisiae (EC=1.1.1.37) Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	Mitochondriel	-1,4	-1,4
SWISSPROT:O74533 Schizosaccharomyces pombe (EC=1.10.2.2) Probable ubiquinol-cytochrome C reductase complex 14 kDa pro	Mitochondriel	-1,4	-1,6

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:O93980 Aspergillus niger CYTOCHROME C OXIDASE SUBUNIT V.	Mitochondriel	-1,4	-2,3
SWISSPROT:P00427 Saccharomyces cerevisiae (EC=1.9.3.1) Cytochrome c oxidase polypeptide VI, mitochondrial precursor	Mitochondriel	-1,5	-1,6
TREMBL:Q8WZW8 Neurospora crassa PROBABLE YHM1 (MITOCHONDRIAL CARRIER).	Mitochondriel	-1,5	-1,2
SWISSPROT:P40086 Saccharomyces cerevisiae Cytochrome c oxidase assembly protein COX15.	Mitochondriel	-1,6	-1,5
TREMBL:Q9P5U4 Neurospora crassa GRPE PROTEIN HOMOLOG.	Mitochondriel	-1,6	-2,5
SWISSPROT:P37211 Neurospora crassa (EC=3.6.3.14) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.	Mitochondriel	-1,6	-1,3
SWISSPROT:P09940 Pichia jadinii ATPase inhibitor, mitochondrial.	Mitochondriel	-1,7	-2,2
SWISSPROT:Q92328 Saccharomyces cerevisiae Mitochondrial inheritance component MDM12.	Mitochondriel	-1,7	-1,3
SWISSPROT:P81449 Saccharomyces cerevisiae (EC=3.6.3.14) ATP synthase e chain, mitochondrial (EC 3.6.3.14).	Mitochondriel	-1,7	-1,3
TREMBL:O94284 Schizosaccharomyces pombe SULFIDE:QUINONE OXIDOREDUCTASE PRECURSOR (EC 1.-.-.-).	Mitochondriel	-1,8	-2,5
SWISSPROT:P56525 Neurospora crassa (EC=3.6.3.14) ATP synthase delta chain, mitochondrial precursor (EC 3.6.3.	Mitochondriel	-1,8	-1,7
SWISSPROT:P56205 Aspergillus niger Cytochrome c.	Mitochondriel	-1,8	-3,1
SWISSPROT:P02723 Neurospora crassa ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucle	Mitochondriel	-1,8	-1,5
TREMBL:O94705 Schizosaccharomyces pombe (EC=1.9.3.1) PUTATIVE CYTOCHROME C OXIDASE POLYPEPTIDE C1259.05C (EC 1.9.	Mitochondriel	-2,1	-2,7
ERDBP:NP000634 Aspergillus oruzae Deduced amino acid sequence for A.oryzae EST AO365 having hi	metabolism	3,0	4,8
ERDBP:NP000634 Aspergillus oruzae Deduced amino acid sequence for A.oryzae EST AO365 having hi	metabolism	2,8	4,8
TREMBL:Q97DL0 Clostridium acetobutylicum AMIDASE FROM NICOTINAMIDASE FAMILY.	metabolism	2,6	11,4
TREMBL:P87017 Aspergillus parasiticus SHORT-CHAIN ALCOHOL DEHYDROGENASE.	metabolism	2,3	2,1
SWISSPROT:P07547 Emericella nidulans (EC=2.5.1.19) Pentafunctional AROM polypeptide [Includes: 3-dehydroquinate	metabolism	2,2	3,5
TREMBL:AAM43715 Dictyostelium discoideum Putative Guanine-nucleotide releasing factor.	metabolism	2,1	2,3
TREMBL:Q9HEE3 Neurospora crassa RELATED TO SORBITOL UTILIZATION PROTEIN SOU1.	metabolism	2,0	3,8
TREMBL:Q96V04 Magnaporthe grisea ACETOLACTATE SYNTHASE SMALL-SUBUNIT-LIKE PROTEIN.	metabolism	2,0	1,2
TREMBL:Q8X1W7 Monascus anka ACID PHOSPHATASE.	metabolism	2,0	1,5
TREMBL:Q9X9X1 Streptomyces coelicolor PUTATIVE ZINC-BINDING DEHYDROGENASE.	metabolism	1,7	1,6
SWISSPROT:P16928 Emericella nidulans (EC=6.2.1.1) Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA liga	metabolism	1,7	1,7
SWISSPROT:Q01278 Neurospora crassa (EC=3.6.3.14) Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E su	metabolism	1,6	1,2
ERDBP:NP000805 Aspergillus niger hemA (5-aminoleveulinate synthase) gene of Aspergillus nige	metabolism	1,5	1,3
TREMBL:Q9P3R9 Neurospora crassa PROBABLE NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLAT	metabolism	1,5	1,4
TREMBL:O14344 Schizosaccharomyces pombe (EC=1.1.1.205) PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.20	metabolism	1,5	3,8
SWISSPROT:Q09751 Schizosaccharomyces pombe (EC=4.4.1.5) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxa	metabolism	1,5	1,3
TREMBL:O74624 Trichoderma reesei (EC=2.7.7.13) MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (MPG1 TR	metabolism	1,5	1,5
GENESEQP:AAY18136 Thielavia terrestris T. terrestris uroporphyrinogen decarboxylase protein sequenc	metabolism	1,4	1,4
GENESEQP:AAM00105 Physcomitrella patens Triosephosphate transporter sequence #173.	metabolism	1,4	2,8
TREMBL:Q12707 Sporobolomyces salmonicolor (EC=1.1.1.2) NADPH-DEPENDENT ALDEHYDE REDUCTASE (EC 1.1.1.2).	metabolism	1,4	1,2
SWISSPROT:Q12657 Penicillium chrysogenum (EC=2.7.1.25) Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine	metabolism	1,3	1,7
TREMBL:Q9Y7D1 Aspergillus terreus TRANSESTERASE.	metabolism	-1,2	-3,4
TREMBL:Q9AGP8 Arthrobacter globiformis N,N-DIMETHYLGLYCINE OXIDASE.	metabolism	-1,5	-1,7
TREMBL:Q9Z4Y6 Streptomyces coelicolor PUTATIVE SALICYLATE HYDROXYLASE.	metabolism	-1,7	-1,9
TREMBL:Q96WL1 Aspergillus parasiticus AFLATOXIN EFFLUX PUMP AFLT.	metabolism	-1,7	-1,4
SWISSPROT:P42882 Aspergillus parasiticus NMT1 protein homolog.	metabolism	-1,9	-4,5
TREMBL:Q9FC45 Streptomyces coelicolor PUTATIVE INTEGRAL MEMBRANE PROTEIN.	membrane	2,2	4,3
TREMBL:Q9P5Y3 Neurospora crassa RELATED TO SYNTAXIN 8.	membrane	1,8	1,9
TREMBL:Q8X090 Neurospora crassa RELATED TO SYNTAXIN 12.	membrane	1,8	1,6
TREMBL:O13312 Aspergillus parasiticus SYNAPTOBREVIN.	membrane	1,5	1,7
TREMBL:Q9P864 Pichia jadinii PUTATIVE MEMBRANE PROTEIN.	membrane	1,5	1,7
TREMBL:Q8X175 Emericella nidulans KARYOPHERIN ALPHA.	membrane	1,4	1,3
TREMBL:O13657 Schizosaccharomyces pombe PROBABLE MEMBRANE PROTEIN YOL130W.	membrane	1,4	1,5

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:Q9UUX8 Neurospora crassa P-TYPE ATPASE (FRAGMENT).	Ion-transport	1,9	2,5
TREMBL:Q9HE83 Neurospora crassa PROBABLE PHOSPHATE TRANSPORT PROTEIN MIR1.	Ion-transport	-1,3	-2,5
TREMBL:Q96TH7 Aspergillus fumigatus PLASMA MEMBRANE H+-ATPASE.	Ion-transport	-1,4	-1,6
TREMBL:O59940 Neurospora crassa CALCIUM/PROTON EXCHANGER.	Ion-transport	-1,4	-4,0
SWISSPROT:Q13733 Homo sapiens (EC=3.6.3.9) Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3	Ion-transport	-1,5	-1,8
TREMBL:Q38998 Arabidopsis thaliana AKT1 POTASSIUM TRANPORTER.	Ion-transport	-1,6	-1,3
TREMBL:Q9HE83 Neurospora crassa PROBABLE PHOSPHATE TRANSPORT PROTEIN MIR1.	Ion-transport	-1,8	-2,4
TREMBL:Q9P426 Ajellomyces capsulata N-GLYCOSYL-TRANSFERASE.	Glycosylering Golgi	1,9	2,0
TREMBL:Q96VV1 Aspergillus awamori PROTEIN O-MANNOSYL TRANSFERASE.	Glycosylering	1,8	1,7
GENESEQP:AAR47201 Saccharomyces cerevisiae DPM2 mannosyl transferase.	Glycosylering	-1,9	-2,0
TREMBL:AAL82734 Aspergillus fumigatus Structural maintenance of chromosome protein.	DNA	2,2	2,4
TREMBL:O14147 Schizosaccharomyces pombe HYPOTHETICAL 96.2 KDA HELICASE C3G6.11 IN CHROMOSOME I	DNA	1,6	2,4
SWISSPROT:Q9P6Q5 Schizosaccharomyces pombe (EC=3.6.1.23) Probable deoxyuridine 5'-triphosphate nucleotidohydrolase(EC	DNA	1,5	1,6
TREMBL:Q8X0K1 Neurospora crassa RELATED TO POL12 (DNA-DIRECTED DNA POLYMERASE ALPHA).	DNA	1,5	1,5
TREMBL:O94395 Schizosaccharomyces pombe PUTATIVE ATP-DEPENDENT DNA HELICASE.	DNA	1,4	1,8
SWISSPROT:Q09176 Schizosaccharomyces pombe Splicing factor U2AF 23 kDa subunit (U2 auxiliary factor 23	DNA	1,4	1,5
SWISSPROT:P48003 Schizosaccharomyces pombe Histone H2A variant.	DNA	1,4	1,2
TREMBL:Q9P3G2 Neurospora crassa (EC=1.17.4.1) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (EC 1.17.4.	DNA	1,3	2,3
TREMBL:CAD37005 Neurospora crassa Related to mismatched base pair and cruciform dna recognitio	DNA	-2,0	-8,9
SWISSPROT:O75001 Schizosaccharomyces pombe DNA replication licensing factor mcm7 (Minichromosome mainte	DNA	-2,6	-1,9
GENESEQP:AAU00959 Fusarium venenatum F. venenatum glucanase polypeptide.	Cell-wall	5,9	4,6
TREMBL:Q9P8U4 Aspergillus fumigatus BETA (1-3) GLUCANOSYLTRANSFERASE GEL2P.	Cell-wall	2,2	2,7
SWISSPROT:Q09196 Schizosaccharomyces pombe Myosin regulatory light chain cdc4.	cell-wall	1,9	1,9
TREMBL:Q9HFQ2 Emericella nidulans (EC=3.1.3.16) PROTEIN PHOSPHATASE 2A.	Cell-wall	1,9	1,5
TREMBL:Q96UK5 Coccidioides immitis BETA-GLUCOSIDASE 5 (FRAGMENT).	Cell-wall	1,9	1,3
TREMBL:Q9P8U4 Aspergillus fumigatus BETA (1-3) GLUCANOSYLTRANSFERASE GEL2P.	Cell-wall	1,8	2,2
TREMBL:Q52423 Pseudomonas sp. ENDO ALPHA-1,4 POLYGALACTOSAMINIDASE PRECUSOR PRECURSOR.	Cell-wall	1,7	3,8
TREMBL:O74687 Aspergillus fumigatus GEL1 PROTEIN.	Cell-wall	1,7	1,6
TREMBL:Q8WZQ2 Neurospora crassa RELATED TO CEL1 PROTEIN.	Cell-wall	1,7	24,2
SWISSPROT:P40414 Saccharomyces cerevisiae Tropomyosin 2.	cell-wall	1,7	1,3
TREMBL:Q92225 Emericella nidulans 1,3-BETA-D-GLUCAN SYNTHASE CATALYTIC SUBUNIT.	Cell-wall	1,7	1,2
TREMBL:Q9C1M3 Emericella nidulans SEPTIN.	cell-wall	1,5	2,3
TREMBL:Q9C1M3 Emericella nidulans SEPTIN.	cell-wall	1,5	1,6
SWISSPROT:Q10133 Schizosaccharomyces pombe Rho2 protein.	Cell-Wall	1,5	2,1
TREMBL:Q9UR09 Schizosaccharomyces pombe CELL WALL SYNTHESIS PROTEIN PSU1	cell-wall	1,5	2,0
TREMBL:AAN00330 Streptococcus agalactiae Cell wall surface anchor family protein	cell-wall	1,4	1,6
TREMBL:Q9P7E8 Schizosaccharomyces pombe ACTIN BINDING PROTEIN WITH SH3 DOMAINS.	Cell-Wall	1,4	1,6
TREMBL:Q9C1M2 Emericella nidulans SEPTIN.	cell-wall	1,4	1,5
TREMBL:Q96VD0 Xanthoria parietina HYDROPHOBIN H1 PRECURSOR.	cell-wall	1,3	1,5
TREMBL:Q9C3Y4 Emericella nidulans RHO GTPASE.	Cell-Wall	1,3	1,5
TREMBL:Q9P302 Emericella nidulans HYPERCELLULAR PROTEIN.	Cell-Wall	-1,4	-1,3
TREMBL:Q9C1L5 Neurospora crassa PUTATIVE RHO GDP DISSOCIATION INHIBITOR G6G8.3	Cell-Wall	-1,4	-1,3
TREMBL:CAD22154 Volvox carteri Pherophorin-dz1 protein.	Cell-Wall	-1,7	-4,6
TREMBL:Q9P8U3 Aspergillus fumigatus BETA (1-3) GLUCANOSYLTRANSFERASE GEL3P (FRAGMENT).	Cell-Wall	-1,9	-2,1
TREMBL:Q07229 Saccharomyces cerevisiae VERPROLIN.	Cell-Wall	-1,9	-31,4
TREMBL:Q9P3F4 Neurospora crassa RELATED TO CHITINASE 3 PRECURSOR PROTEIN.	Cell-Wall	-2,2	-2,6
SWISSPROT:Q04951 Saccharomyces cerevisiae Probable family 17 glucosidase SCW10 precursor (EC 3.2.1.-)	Cell-Wall	-2,3	1,5
TREMBL:AAC49609 Saccharomyces diastaticus Glucoamylase.	Carbon-metabolism	2,5	1,2
TREMBL:Q96WT4 Aspergillus oryzae MALTASE.	Carbon-metabolism	2,3	5,9
GENESEQP:AAW88044 Acremonium sp. An enzyme with sugar transferase activity.	Carbon-metabolism	1,9	2,3

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
GENESEQP:AAY56815 Bacillus sp. Bacillus D-arabinitol dehydrogenase.	Carbon-metabolism	1,9	1,4
TREMBL:Q9P8R5 Aspergillus niger D-XYLOSE REDUCTASE.	Carbon-metabolism	1,6	1,6
TREMBL:AAM46059 Oryza sativa Putative aldose 1-epimerase-like protein.	Carbon-metabolism	1,6	3,5
SWISSPROT:P50166 Candida tropicalis (EC=1.1.1.250) D-arabinitol 2-dehydrogenase [ribulose forming] (EC 1.1.1.25	Carbon-metabolism	1,6	2,5
TREMBL:Q9TEM3 Emericella nidulans (EC=4.1.3.31) METHYLCITRATE SYNTHASE PRECURSOR (EC 4.1.3.31).	Carbon-metabolism	1,6	1,4
TREMBL:Q9URW9 Schizosaccharomyces pombe PROBABLE ALDEHYDE DEHYDROGENASE.	Carbon-metabolism	1,5	1,2
SWISSPROT:P44538 Haemophilus influenzae (EC=3.5.99.6) Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Glucosamine	Carbon-metabolism	1,4	3,1
TREMBL:CAD36981 Neurospora crassa Related to glucosidase II, alpha subunit.	Carbon-metabolism	1,4	1,8
TREMBL:Q9HGZ3 Aspergillus oryzae HEXOKINASE.	Carbon-metabolism	1,4	1,5
GENESEQP:AAR70209 Aspergillus niger A. niger alpha-galactosidase.	Carbon-metabolism	1,3	3,1
TREMBL:Q9P8D6 Aspergillus niger (EC=4.1.3.7) CITRATE SYNTHASE PRECURSOR (EC 4.1.3.7).	Carbon-metabolism	-1,2	-1,9
TREMBL:Q9HGY8 Aspergillus oryzae (EC=5.3.1.1) TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM).	Carbon-metabolism	-1,3	-2,8
TREMBL:Q9HGY7 Aspergillus oryzae GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.	Carbon-metabolism	-1,3	-1,8
SWISSPROT:Q12560 Aspergillus oryzae (EC=4.2.1.11) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-ph	Carbon-metabolism	-1,4	-1,4
TREMBL:Q9C415 Aspergillus oryzae (EC=1.2.1.12) GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12).	Carbon-metabolism	-1,4	-2,1
SWISSPROT:O13309 Pichia stipitis (EC=1.1.1.1) Alcohol dehydrogenase II (EC 1.1.1.1) (ADH 1).	Carbon-metabolism	-1,4	-1,5
TREMBL:Q9C253 Neurospora crassa PROBABLE GLYCERONE KINASE ISOFORM.	Carbon-metabolism	-1,5	-1,3
TREMBL:Q9P8D6 Aspergillus niger (EC=4.1.3.7) CITRATE SYNTHASE PRECURSOR (EC 4.1.3.7).	Carbon-metabolism	-1,7	-2,8
TREMBL:Q9HE50 Neurospora crassa RELATED TO MALATE DEHYDROGENASE (OXALOACETATE-DECARBOXYLATIN	Carbon-metabolism	-1,8	-1,6
TREMBL:O94185 Aspergillus oryzae PYRUVATE DECARBOXYLASE.	Carbon-metabolism	-2,2	-7,3
ERDBP:NP000614 Aspergillus oruzae Deduced amino acid sequence for A.oryzae EST AS1789 having h	AO EST	1,6	1,4
ERDBP:NP000292 Aspergillus oryzae Deduced amino acid sequence of genomic DNA sequence encoding	AO EST	-2,3	-3,8